

PURIFIED INSOLUBLE FRACTION  
His COLUMN-PASSAGE FRACTION  
His COLUMN BINDING/ELUTED FRACTION

ENRICHED FRACTION AFTER DIALYSIS  
(FINAL PURIFICATION PRODUCT)

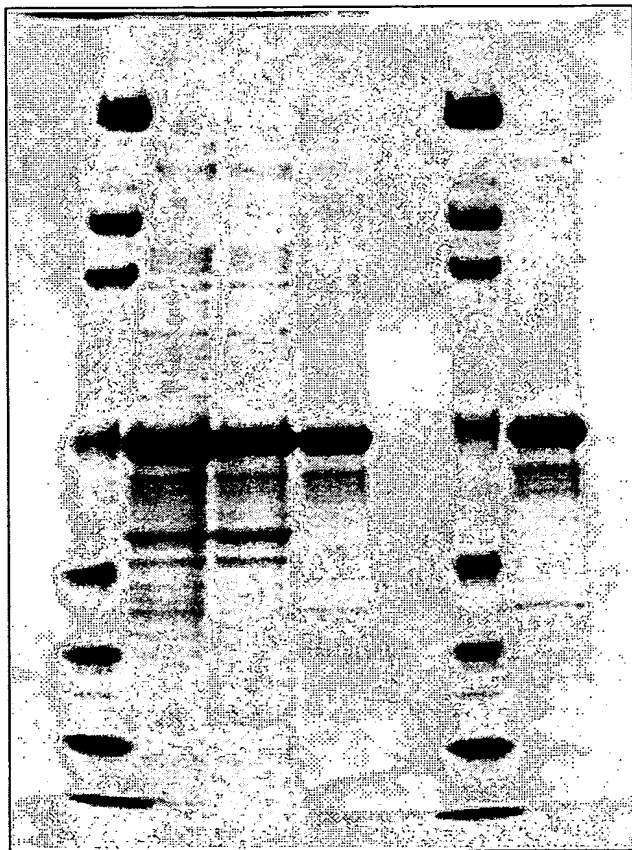


FIG. 1

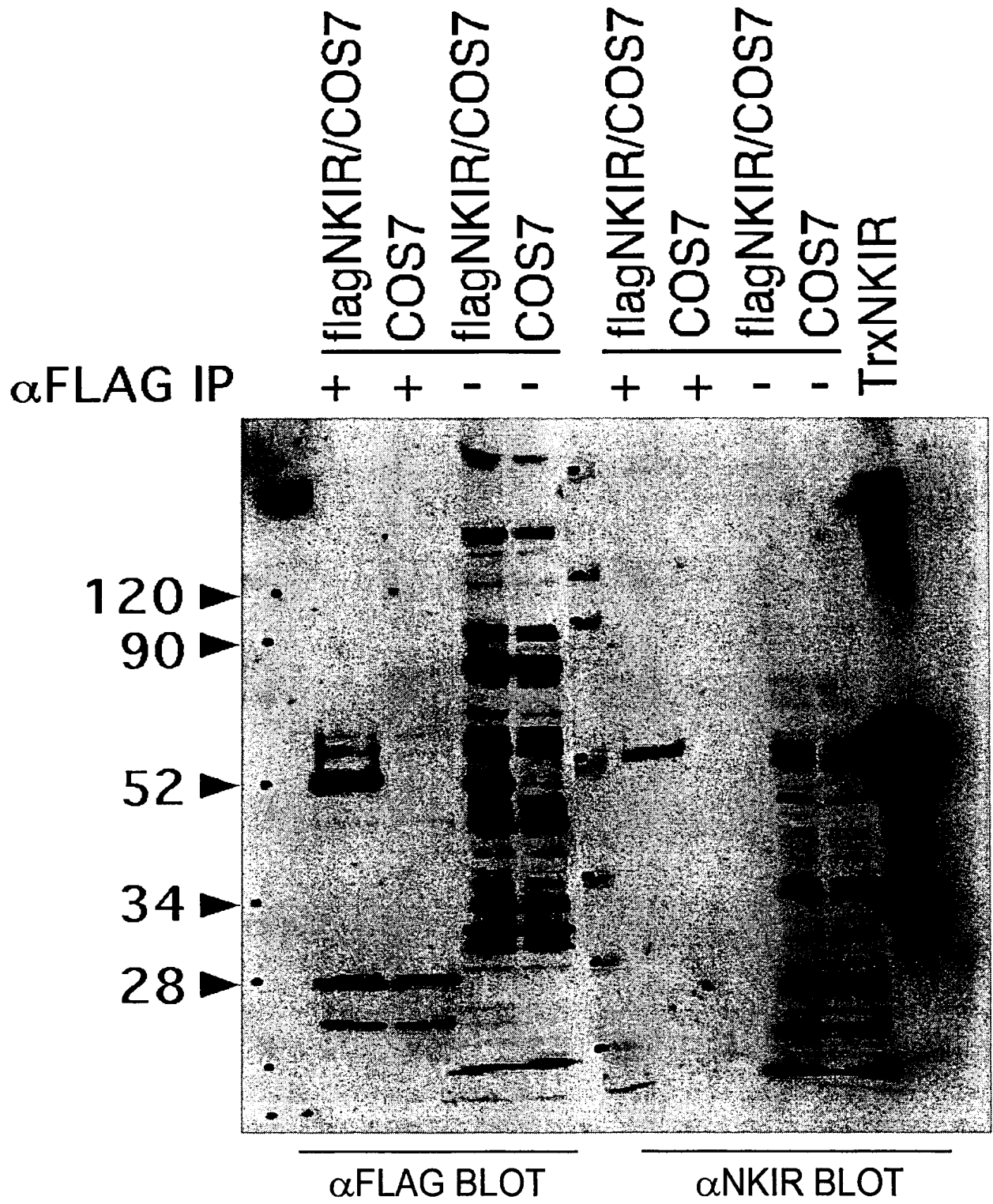


FIG. 2

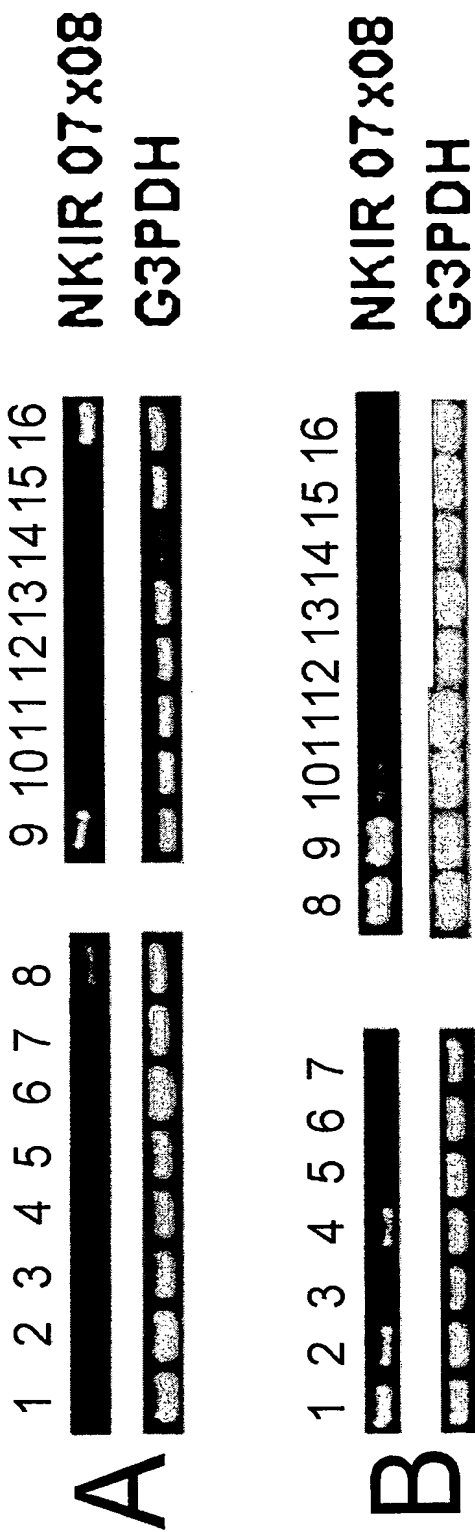


FIG. 3

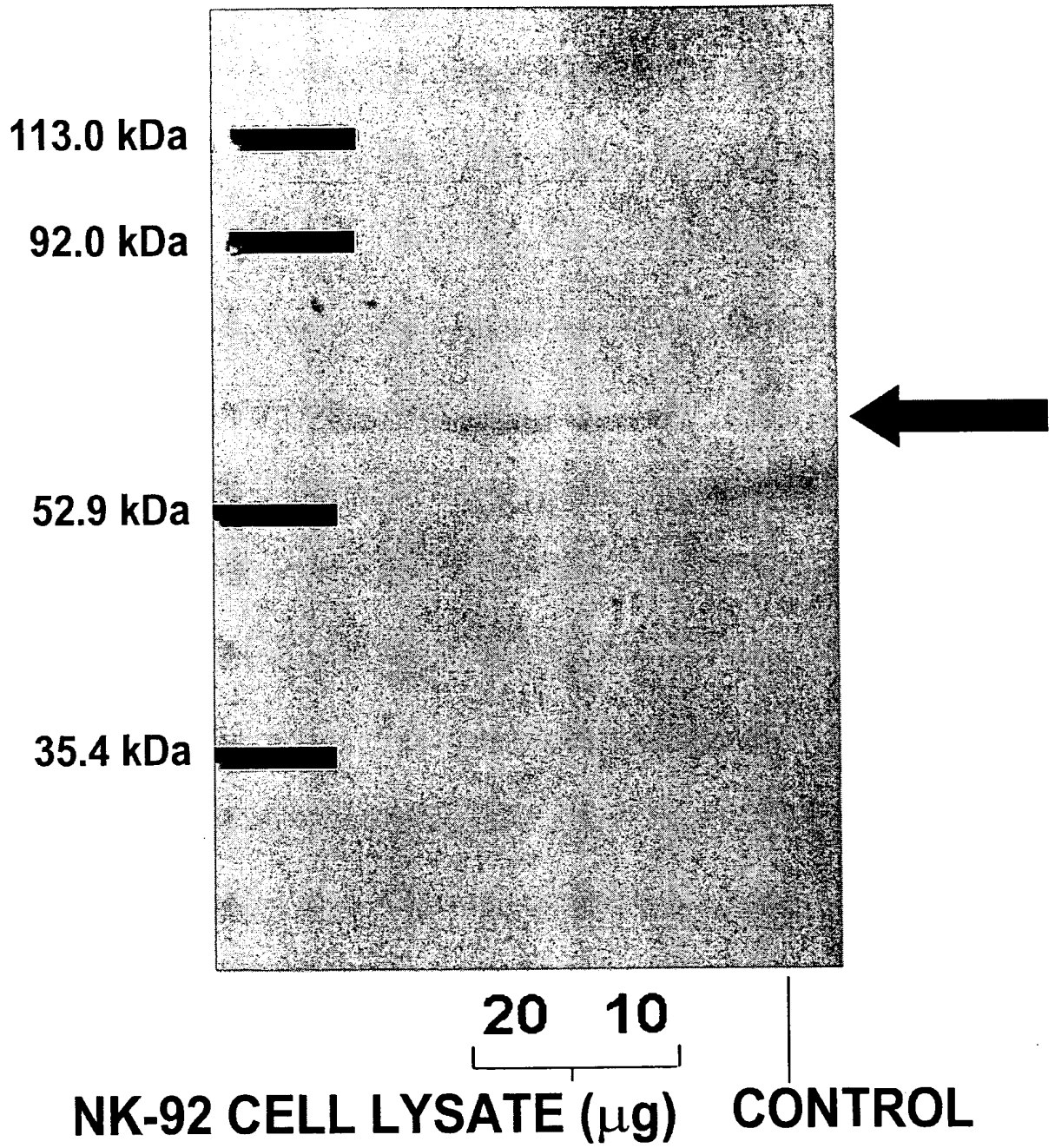


FIG. 4

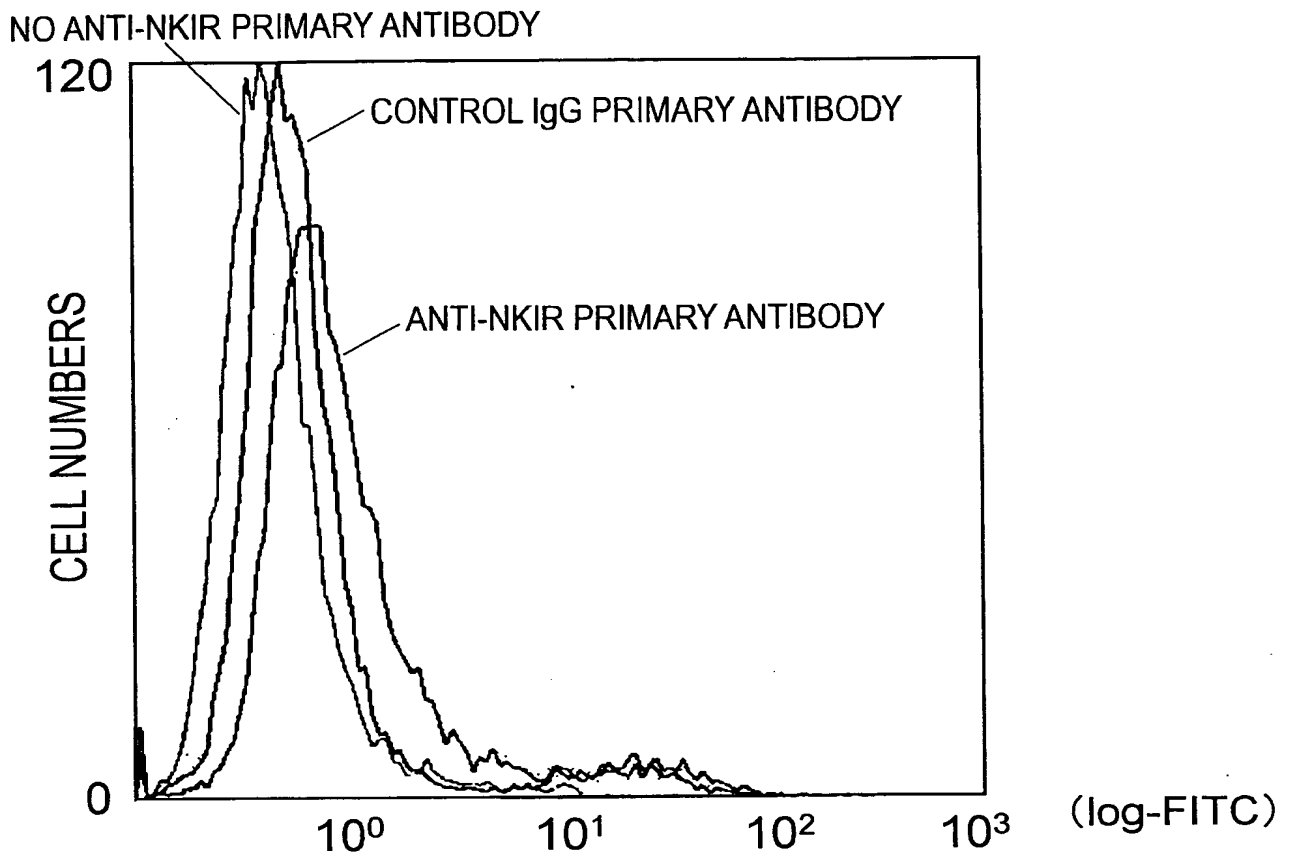
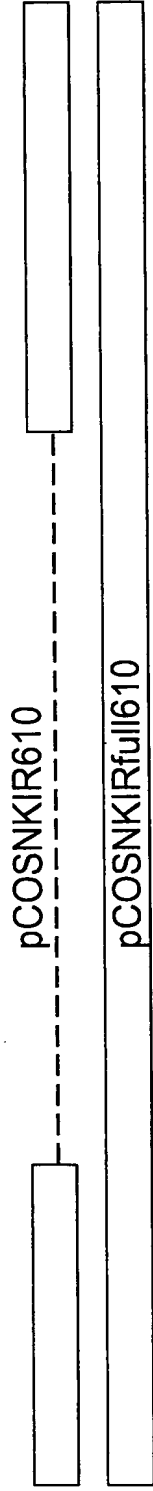


FIG. 5

ATGTTGCCATCTTTAGGGCCCCCATGCTGCTCTGGACGGCTGTGCTCTTTGTTCCCTGTGTGGGAAA  
 M L P S L G P M L L L W T A V L L F V P C V G K



VECTOR BACKBONE: pCOS1

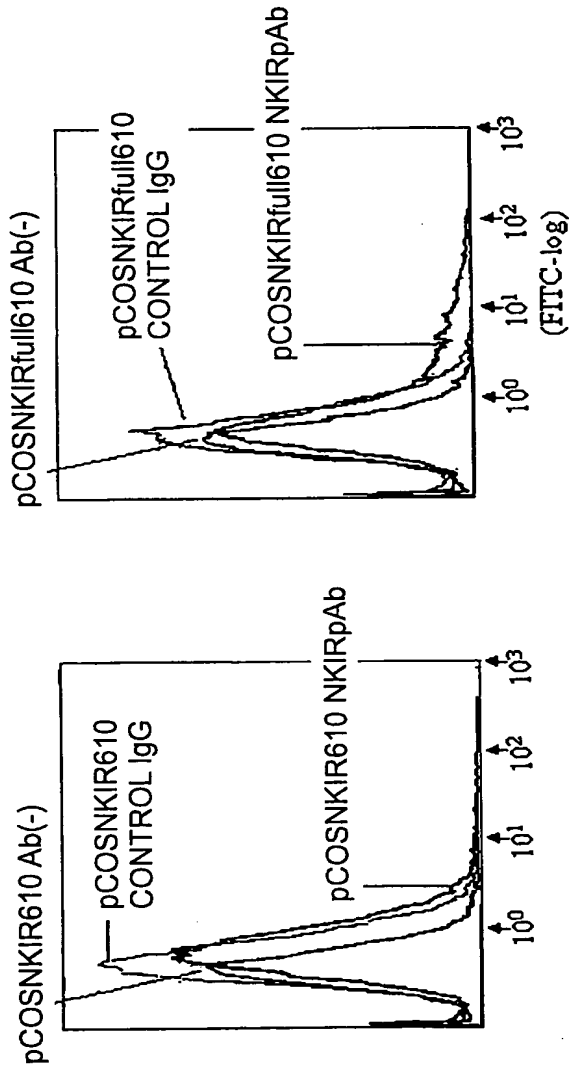


FIG. 6

FIG. 7

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Score = 263 (92.6 bits), Expect = 1.9e-28, Sum P(3) = 1.9e-28  
Identities = 62/369 (50%), Positives = 78/369 (63%), Frame = -3

Query: 197 APVSRPVLTLHHGPADPAVGMVQLLCEAQRGSPPILYSFYLDEKIVGNHSAPCGGTTSL 256

APVS PVLTL H + AVGD V+ LCEA +GS PI YSFY++ +I+G AP G SL

Sbjct: 891239 APVSHPVLTQLQHEATNLAVGDKVEFLCEAHQGSLLPIFYSFYINGEILGKPLAPSGRAASL  
891060

EXTRACELLULAR  
CANDIDATE REGION

Query: 257 LFPVKSEQDAGNYSCEAENSVSRRSEPKKLSLKGSQL--FTPA 299

L VK+E NYSCEA+N++SRE SE KK L G + +TP

Sbjct: 891059 LASVKAEWSTKNYSCEAKNNISREISELKKFPLVGMFCIIISYTPV 980924  
EXON AT POSITION N

Score = 82 (28.9 bits), Expect = 1.9e-28, Sum P(3) = 1.9e-28  
Identities = 18/75 (72%), Positives = 20/75 (80%), Frame = -2

Query: 300 SNWLVPWLPASLLGLMVIAAALLVY 324

SN L WLPASLLG MVIAA +L+Y

Sbjct: 890637 SNMLPIWLPASLLGGMVIAAVVLMY 890563

TRANSMEMBRANE REGION

EXON AT POSITION N+1

```

mNKIR -----
hNKIR MLPSLPCVGVKTVWLYLQAWPNPVFEGDALTLRCQGWKNTPLSQVKFYRDGKFLHFSKEN

mNKIR -----MLL-WMVPLLCDS-MVEAQELFPNPELTFEFTNSETMD-
hNKIR QTLSMGAATVQSRGQYSCSGQVMYIPQTFTQTSAMVQVQELFPPPLSAIPSEPREG
      *:::      :: **::***** * **:::***. *
mNKIR --VILKCTIKVDPKNPTLQLFYTFYKDNHVIQDRSPH-SVFSAAKEENSGLYQCMVDTE
hNKIR SLVTLRCQTKLHPLRSALRLLFSFHKDGHHTLQDRGHPHELCPGAKEGDSGLYWCEVAPE
      * ** * *::: * *:::***::***. * . *** :***** * * *
mNKIR DGLIQKKSGYLDIQFWTPVSHPVLTLLQHEATNLAVGDKVEFLCEAHQGSGLPIFYSFYING
hNKIR GGQVQKQSPQLEVRVQAPVSRPVLTLHHGPADPAVGDMVQLLCEAQRGSPPILYSFYLDE
      * :***: * *::: * :***:*****: * :: ***** *::*****:
mNKIR EILGKLAPSGRAASLLASVKAEWSTKNYSCEAKNNISREISELKKFPLVVSGETAWIKS-
hNKIR KIVGNHSAPCGGTTSLFPVKSEQDAGNYSCEAENSVSRESERSEPKKLSLKGSQLFTPAS
      :*: * * * :***. *:: * : *****: *::*** * * * * : :
mNKIR NMLTIWLPASLLGGMVIAAVLVMYFFKPKCKKHARLEMP TLKEPDS--FLYVSVDNRRYK
hNKIR NWLVPWL PASLLGLMVIAAALLVYVRSWRKAGPLPSQIPPTAPGGEQCPLYANVHHQKKGK
      * * ***** *::: * . * . . * . * . * . *
mNKIR -----
hNKIR DEGVVYSVVHRTSKRSEARSAEFTVGRKDSII CAEVRCLQPSEVSSTEVMRSTRTLQEP

mNKIR -----
hNKIR LSDCEEVLC

```



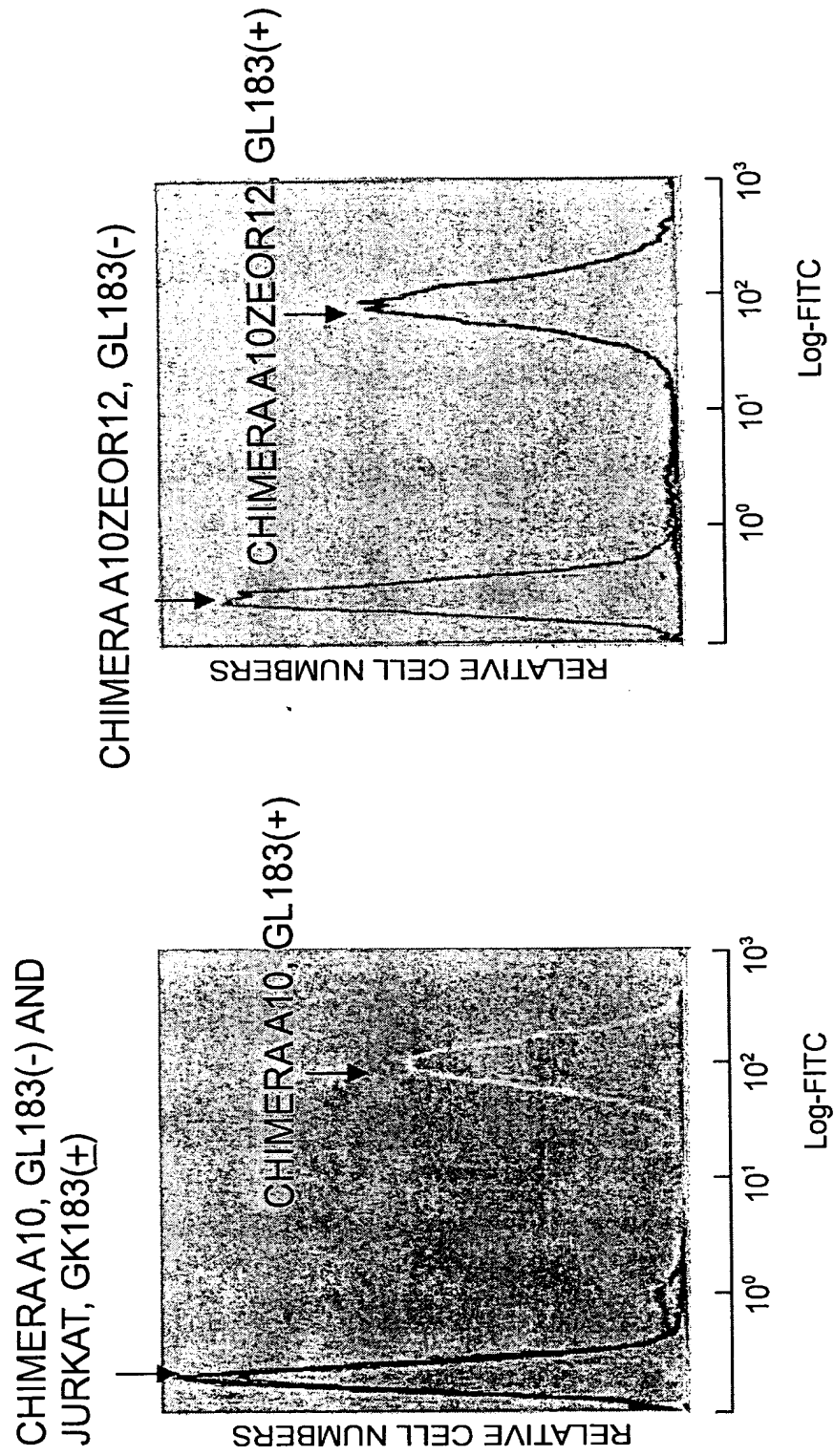


FIG. 9

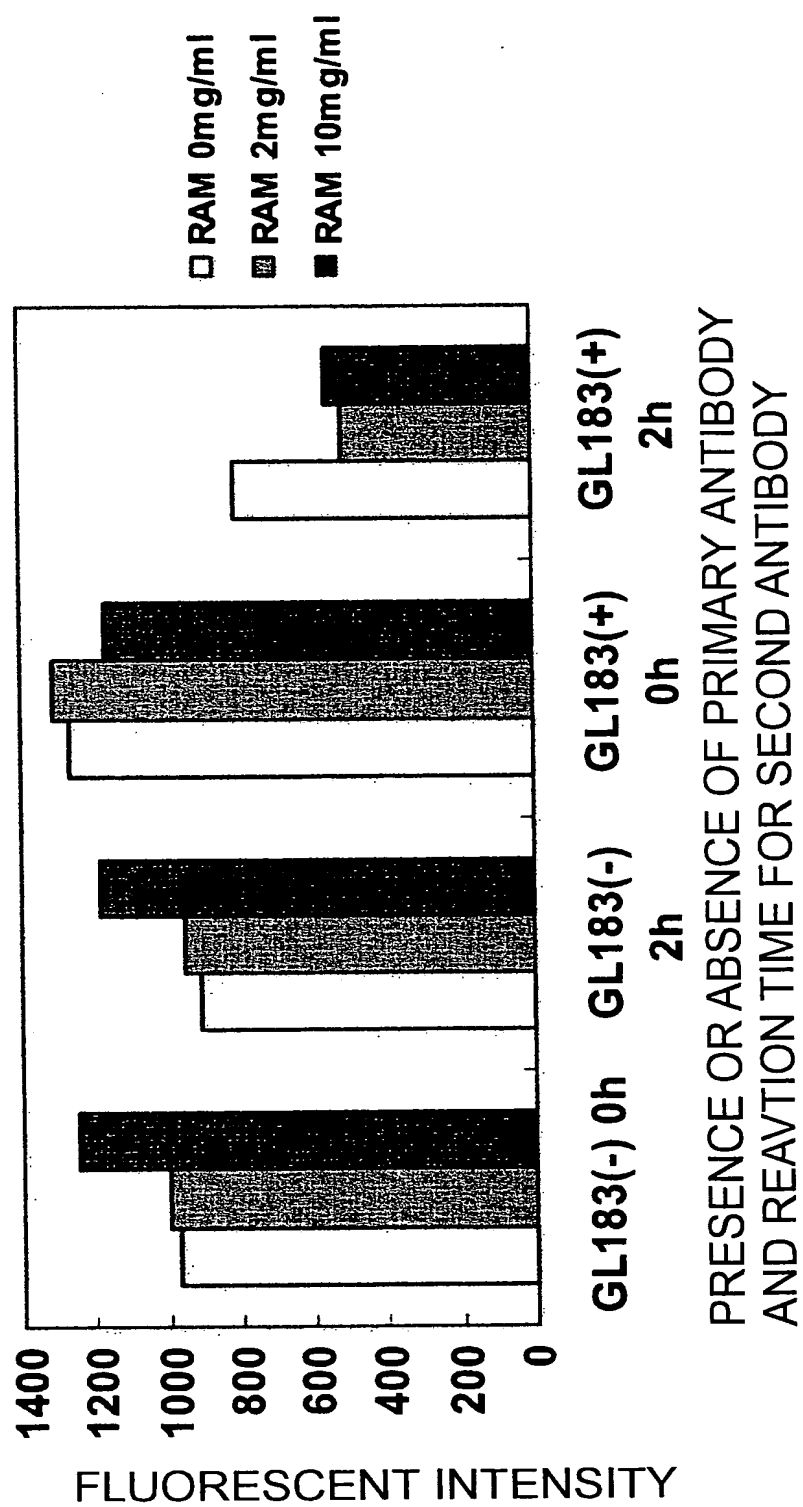


FIG. 10

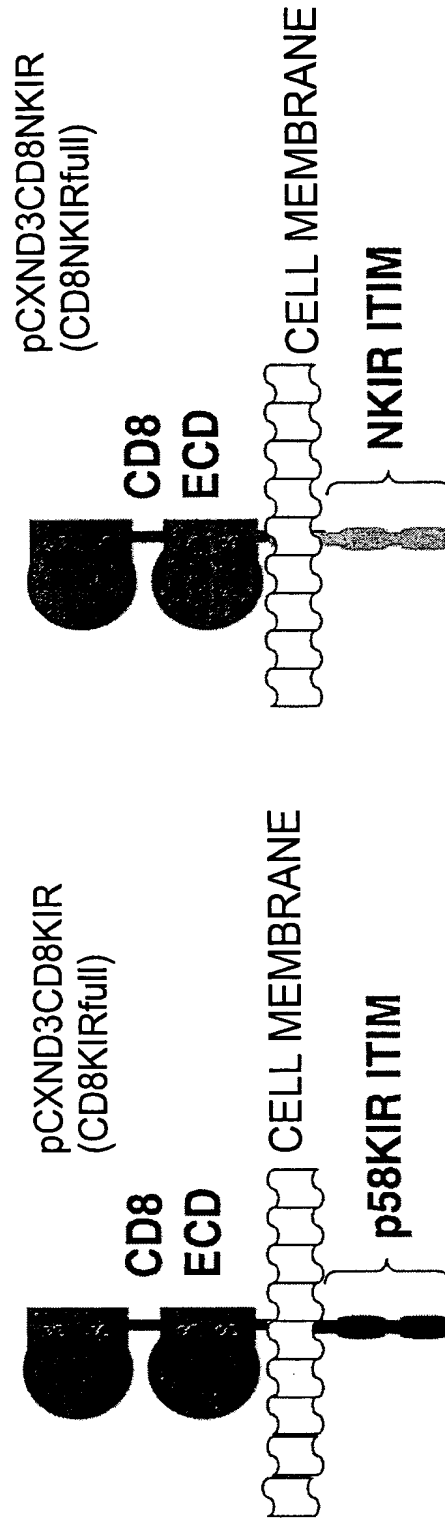


FIG. 11-1

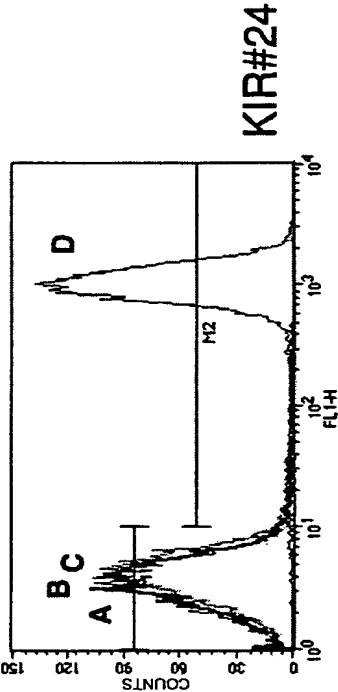
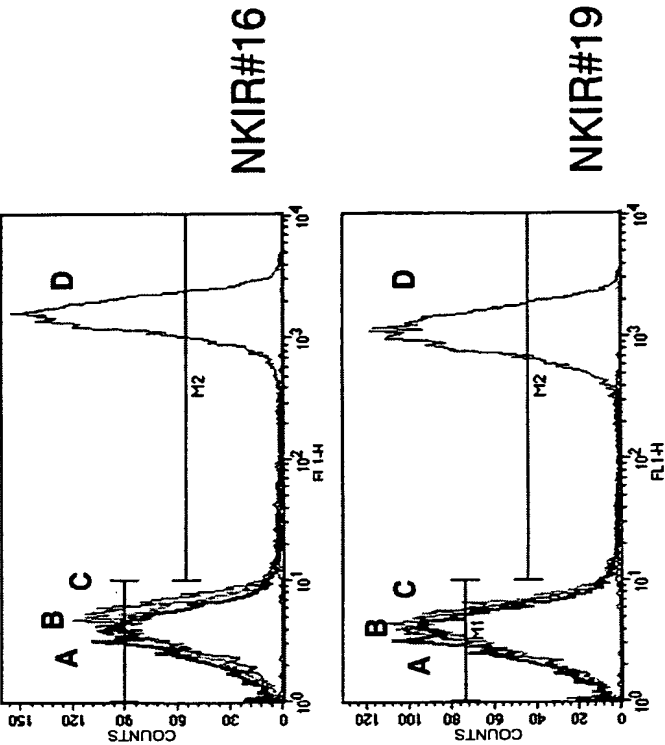


FIG. 11-2

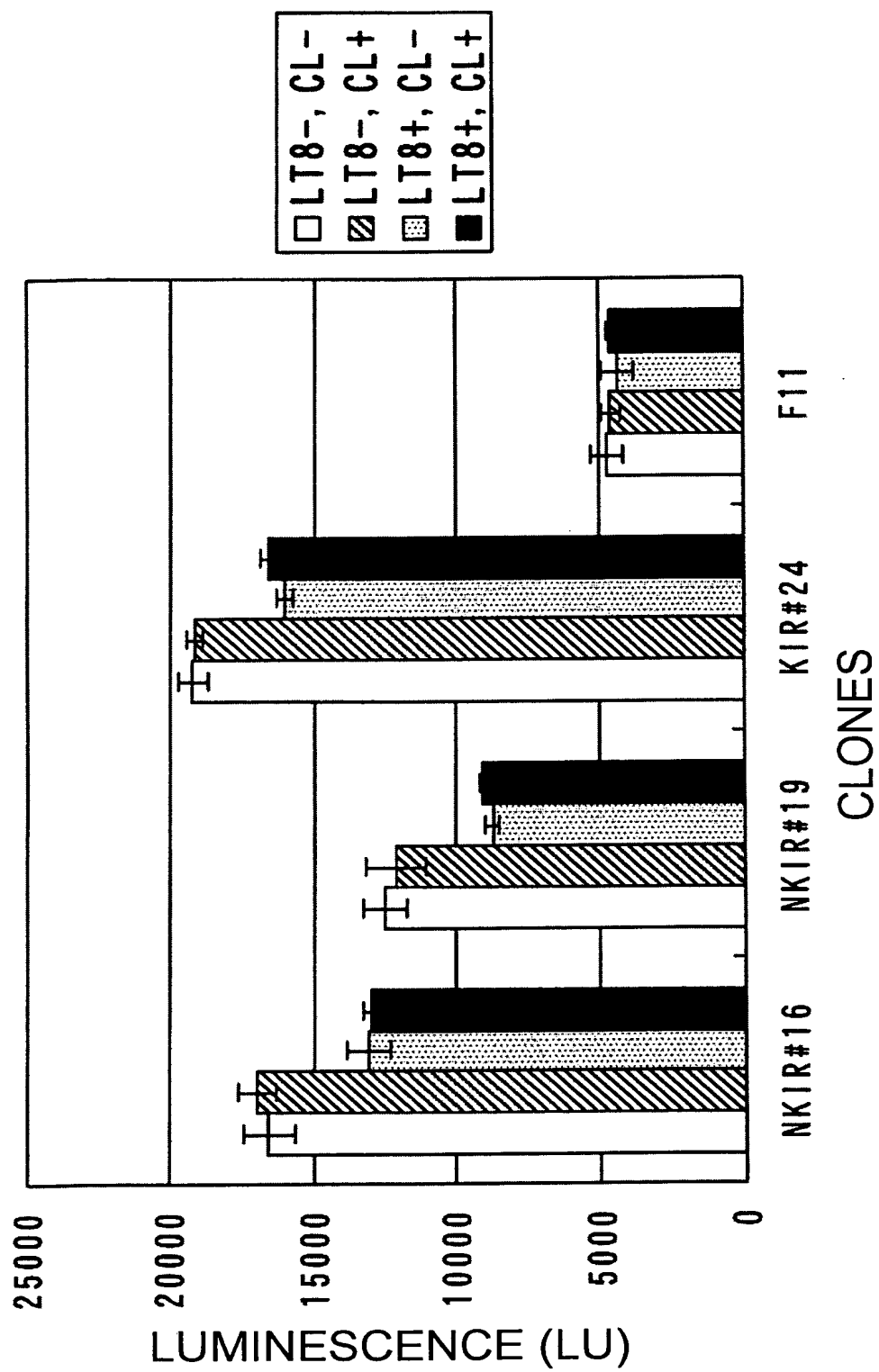


FIG. 12